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SEQUENCE LISTING

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Jønson, Lars
5 Rehfeld, Jens F.
Johnsen, Anders H.

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a recombinant polypeptide from a host cell
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35 40 45

45 His Ser Gln Thr Gly Ala Glu His Leu His Ile Asp Arg Asp Asp Lys
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Gly Val Pro His Ile Leu Glu His Thr Thr Leu Cys Gly Ser Val Lys
55 85 90 95

Tyr Pro Val Arg Asp Pro Phe Phe Lys Met Leu Asn Lys Ser Leu Ala
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Asp	Ser	Thr	Leu	Asn	Pro	Leu	Leu	Lys	Gln	Glu	Asp	Phe	Asp	Gln
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Gly	Trp	Arg	Leu	Glu	His	Lys	Asn	Ile	Thr	Asp	Pro	Glu	Ser	Asn
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Val	Phe	Lys	Gly	Val	Val	Tyr	Asn	Glu	Met	Lys	Gly	Gln	Ile	Ser
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Tyr	Gln	Lys	Leu	Ile	Glu	Ser	Gly	Ile	Gly	Leu	Glu	Phe	Ser	Val
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Ser Gly Val Glu Pro Thr Thr Ala Val Asn Leu Leu Thr Val Gly Ile
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Gln Gly Val Ser Asp Ile Glu Ile Phe Lys Asp Thr Val Asn Asn Ile
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Phe Gln Asn Leu Leu Glu Thr Glu His Pro Phe Asp Arg Lys Arg Ile
 385 390 395 400

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Asp Ala Ile Ile Glu Gln Leu Glu Leu Ser Lys Lys Asp Gln Lys Ala
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Lys Ile Asp Pro Phe Glu Ser Leu Leu Phe Glu Asp Val Leu Gln Arg
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Phe Arg Gly Asp Leu Glu Thr Lys Gly Asp Thr Leu Phe Gln Asp Leu
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Ile Arg Lys Tyr Ile Val His Lys Pro Cys Phe Thr Phe Ser Ile Gln
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Gly Ser Glu Glu Phe Ser Lys Ser Leu Asp Asp Glu Glu Gln Thr Arg
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Asp Thr Asn Gly Ile Thr Tyr Val Arg Gly Lys Arg Leu Leu Asn Asp
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Ser Asp Pro Asn Thr Thr Glu Pro Arg Leu Ile Phe Gly Phe Asp Gly
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25 Gly His Ala Phe Ala Arg Gly Tyr Ser Ala Ala His Tyr Arg Ser Ser
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Val Val Asp Lys Leu Thr Glu Leu Gln Lys Tyr Ile Val Asp Thr Asn
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Cys Leu Pro Asn Gly Pro Lys Thr Ser Asp Tyr Pro Leu Ile Gly Ser
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Leu Gln Val Met Ser Asn Met Leu Thr Phe Lys His Leu His Arg Glu

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70 Leu Asn Tyr Thr Arg Leu Lys His Glu Pro Thr Asn Ala Asp Met Ile
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Pro Phe Ser Lys Arg Glu Leu Asn Leu Pro Asn Thr Phe Leu Lys Glu
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Ser Leu Ala Lys Ile Glu Asn Leu Val Tyr Ser Ile Phe Asn Asp Leu
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Tyr Ala Leu Ser Ser Gly Gly Asp Pro Asp Glu Ile Pro Asn Leu Thr
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Pro Leu Lys Lys Ala Leu Ile Asp Ala Gly Ile Gly Lys Ala Val Ser
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Gly Asp Phe Asp Asn Ser Thr Lys Gln Ser Ala Phe Thr Val Leu Val
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Leu Glu Lys Ile Lys Ser Ala Leu Thr Ser Asn Tyr Phe Glu Asp Leu
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 485 490 495

40 Ile Ile Asp Asn Cys Lys Lys Leu Lys Glu Arg Gln Ser Thr Pro Asp
 500 505 510

Lys Lys Glu Asp Leu Glu Ser Ile Pro Met Leu Ser Leu Glu Asp Ile
 515 520 525

45 Asp Lys Glu Ala Thr Lys Ile Pro Thr Glu Glu Lys Glu Ile Asp Gly
 530 535 540

Ile Thr Thr Leu His His Asp Phe His Thr Asn Lys Ile Asp Tyr Val
 545 550 555 560

50 Asn Phe Phe Phe Asn Thr Asn Ser Val Pro Glu Asp Leu Ile Pro Tyr
 565 570 575

55 Val Gly Leu Leu Cys Asp Ile Leu Gly Lys Cys Gly Thr Glu Asn Tyr
 580 585 590

20/67

Asp Tyr Ser Lys Leu Ser Asn Ala Ile Asn Ile Ser Thr Gly Gly Ile
 595 600 605

5 Ser Phe Gly Ala Ile Thr Phe Ala Asn Leu Lys Lys Asn Asn Glu Phe
 610 615 620

10 Arg Pro Tyr Leu Glu Ile Ser Tyr Lys Ala Leu Ser Ser Lys Thr Asn
 625 630 635 640

15 Lys Ala Ile Glu Leu Val Asp Glu Ile Val Asn His Thr Asp Leu Asp
 645 650 655

Asp Met Asp Arg Ile Met Gln Ile Ile Arg Glu Lys Arg Ala Arg Leu
 660 665 670

20 Glu Gly Ala Ile Phe Asp Ser Gly His Arg Ile Ala Met Lys Lys Val
 675 680 685

25 Leu Ser Tyr Ser Thr Asn Arg Gly Ala Tyr Asp Glu Lys Ile Ser Gly
 690 695 700

30 Leu Asp Tyr Tyr Asp Phe Leu Val Asn Ile Glu Lys Glu Asp Lys Lys
 705 710 715 720

35 Ser Thr Ile Ser Asp Ser Leu Lys Lys Val Arg Asp Leu Ile Phe Asn
 725 730 735

40 Lys Gly Asn Met Leu Ile Ser Tyr Ser Gly Lys Glu Glu Glu Tyr Glu
 740 745 750

Asn Phe Lys Glu Lys Val Lys Tyr Leu Ile Ser Lys Thr Asn Asn Asn
 755 760 765

45 Asp Phe Glu Lys Glu Glu Tyr Asn Phe Glu Leu Gly Lys Lys Asn Glu
 770 775 780
 Gly Leu Leu Thr Gln Gly Asn Val Gln Tyr Val Ala Lys Gly Gly Asn
 785 790 795 800

50 Tyr Lys Thr His Gly Tyr Lys Tyr Ser Gly Ala Leu Ser Leu Leu Glu
 805 810 815

55 Ser Ile Leu Gly Phe Asp Tyr Leu Trp Asn Ala Val Arg Val Lys Gly
 820 825 830

Gly Ala Tyr Gly Val Phe Ser Asn Phe Arg Arg Asp Gly Gly Ala Tyr

21/67

835

840

845

5 Ile Val Ser Tyr Arg Asp Pro Asn Ile Lys Ser Thr Leu Glu Ala Tyr
 850 855 860

10 Asp Asn Ile Pro Lys Tyr Leu Asn Asp Phe Glu Ala Asp Glu Arg Glu
 865 870 875 880

15 Met Thr Lys Tyr Ile Ile Gly Thr Ile Arg Lys Tyr Asp Gln Pro Ile
 885 890 895

20 Ser Asn Gly Ile Lys Gly Asp Ile Ala Val Ser Tyr Tyr Leu Ser Asn
 900 905 910

25 Phe Thr Tyr Glu Asp Leu Gln Lys Glu Arg Glu Glu Ile Ile Asn Ala
 915 920 925

30 Asp Val Glu Lys Ile Lys Ser Phe Ala Pro Met Ile Lys Asp Leu Met
 930 935 940

35 Lys Glu Asp Tyr Ile Cys Val Leu Gly Asn Glu Glu Lys Ile Lys Glu
 945 950 955 960

40 Asn Lys Asp Leu Phe Asn Asn Ile Lys Ser Val Ile Lys
 965 970

<210> 7
 <211> 971
 <212> PRT
 <213> Borrelia burgdorferi

45 Met Lys Lys Lys Lys Ile Phe Lys Leu Ile Ser Lys Thr Tyr Leu Glu
 1 5 10 15

50 Glu His Asp Ala Glu Gly Tyr Tyr Phe Lys His Glu Ser Gly Leu Glu
 20 25 30

55 Val Phe His Leu Lys Ser Asp Ser Phe Lys Glu Asn Ala Phe Cys Ile
 35 40 45

60 Ala Phe Lys Thr Ile Pro Ser Asn Asn Thr Gly Val Ala His Val Leu
 50 55 60

65 Glu His Thr Ile Phe Cys Gly Ser Ser Lys Tyr Lys Ile Lys Asp Pro
 65 70 75 80

22/67

5 Phe Leu Tyr Leu Leu Lys Gly Ser Leu Asn Thr Phe Leu Asn Ala Met
85 90 95

10 Thr Phe Pro Asp Lys Thr Ile Tyr Pro Ala Ala Ser Thr Ile Glu Lys
100 105 110

15 Asp Tyr Phe Asn Leu Phe Asn Ile Tyr Ala Asp Ser Ile Phe Asn Pro
115 120 125

20 Lys Asp Phe Lys Val Ser Gly Ile Val Phe Asn Glu Met Lys Gly Ser
145 150 155 160

25 Tyr Ser Asn Lys Asn Ser Leu Ile Asn Glu Ile Val Ser Ser Ser Leu
165 170 175

30 Phe Glu Glu Gly Ala Tyr Lys Tyr Asp Ser Gly Gly Ile Pro Thr Asn
180 185 190

35 Ile Ile Asp Leu Thr Tyr Glu Ser Phe Leu Asp Phe Tyr Lys Lys Tyr
195 200 205

40 Glu Lys Asn Leu Asn Phe Ile Glu Lys Tyr Ile Ile Arg Pro Tyr Lys
225 230 235 240

45 Lys Glu Lys Ser Asn Val Asn Ile Asn Ile Glu Asn Val Lys Arg Trp
245 250 255

50 Glu Lys Gly Lys Lys Leu Thr Tyr Lys Ile Pro Lys Glu Asn Asp Asn
260 265 270

55 Ser Leu Gly Val Tyr Thr Ile Asn Trp Leu Cys Thr Glu Ile Asn Asn
275 280 285

Ile Glu Asp Ser Ile Gly Leu Glu Ile Leu Ser Glu Ile Leu Leu Asp
290 295 300

Asp Ser Cys Ser Phe Thr Ile Asn Ile Leu Lys Ser Gly Ile Gly Glu
305 310 315 320

23/67

Asp Ile Ala His Ile Ser Gly Ile Asn Thr Asp Leu Lys Glu Ser Ile
 325 330 335
 5
 Phe Ser Phe Gly Leu Gln Asn Val Val Glu Asn Lys Glu Lys Glu Phe
 340 345 350
 10 Lys Asn Leu Val Phe Ser Glu Leu Lys Asn Leu Val Lys Asn Lys Ile
 355 360 365
 Pro Lys Glu Leu Ile Lys Gly Ile Leu Phe Gly Tyr Glu Phe Ala Leu
 15 370 375 380
 Lys Glu Glu Lys Gly Gln Asn Phe Pro Ile Ala Leu Met Ile Lys Ser
 20 385 390 395 400
 Phe Lys Gly Trp Leu Asn Gly Leu His Pro Ile Lys Thr Leu Gln Thr
 405 410 415
 25
 Ser Tyr Tyr Ile Asn Glu Ile Thr Asn Lys Leu Glu Lys Gly Ile Tyr
 420 425 430
 30 Tyr Phe Glu Asn Leu Ile Glu Lys Tyr Leu Ile Phe Asn Asn His Tyr
 435 440 445
 Thr Leu Ile Ser Phe Ile Pro Ser His Asp Thr Glu Lys Glu Met Glu
 35 450 455 460
 Glu Glu Ile Glu Lys Lys Leu Met Ala Arg Glu Ile Glu Ile Lys Gln
 40 465 470 475 480
 Asn Pro Glu Glu Phe Leu Gln Phe Lys Lys Asp Tyr Asn Gln Phe Lys
 485 490 495
 45 Lys Tyr Gln Asn Lys Lys Asp Ser Lys Ala Asp Ile Ala Lys Leu Pro
 500 505 510
 Leu Leu Lys Ile Glu Asp Leu Pro Lys Gln Ile Glu Lys Ser Leu Asp
 50 515 520 525
 Leu Asn Glu Ile Lys Glu Leu Asn Leu His Ser Phe Lys Phe Lys Ser
 530 535 540
 55
 Asn Asn Ile Phe Asn Val Asn Leu Phe Phe Lys Leu Asp Phe Leu Glu
 545 550 555 560

24/67

Lys Glu Asp Tyr Ile Tyr Leu Ser Leu Phe Lys Arg Ala Leu Gln Asp
 565 570 575

5 Leu Ser Thr Lys Asn Tyr Ser Tyr Ile Asn Ile Asn Asn Lys Ile Gln
 580 585 590

10 Asn Thr Leu Gly Gln Ile Asn Ile Ser Glu Ser Tyr Asp Glu Asp Ile
 595 600 605

15 Asp Gly Asn Ile Leu Asn Ser Phe Asn Ile Ser Phe Lys Ser Phe Asn
 610 615 620

Asn Lys Val Lys Glu Ser Phe Glu Leu Ile Lys Glu Ile Leu Ile Asn
 625 630 635 640

20 Ile Asn Phe His Asp Tyr Glu Arg Leu Lys Glu Ile Thr Leu Ser Leu
 645 650 655

25 Lys Asn Asp Phe Lys Ser Leu Leu Ile Pro Lys Gly His Leu Leu Ala
 660 665 670

30 Met Leu Arg Ser Lys Ser Lys Leu Lys Leu Asn Glu Tyr Leu Lys Glu
 675 680 685

Leu Gln Asn Gly Ile Thr Gly Arg Glu Phe Trp Gln Lys Ala Lys Thr
 690 695 700

35 Asp Thr Glu Ser Leu Lys Glu Ile Ala Asn Lys Leu Asp Asn Leu Lys
 705 710 715 720

40 Asn Lys Ile Ile Leu Lys Asn Asn Leu Ser Ala Leu Ile Met Gly Asn
 725 730 735

Thr Asp Asp Ile Leu Lys Asn Leu Glu Asn Glu Phe Phe Asn Leu Lys
 740 745 750

45 Glu Ser Leu Glu Glu Ser Asn His Tyr Asn Gly Leu Leu Asn Leu Asp
 755 760 765

50 Ala Asn Ser Lys Ala Leu Arg Glu Ile Ile Ile Ile Gln Ser Lys Val
 770 775 780

55 Ala Phe Asn Ala Ile Cys Phe Pro Ser Tyr Lys Ile Asn Asp Glu Asn
 785 790 795 800

Tyr Pro Lys Ala Asn Phe Leu Glu His Val Leu Arg Ser Gly Ile Phe

805

810

815

5

10

15

35

<400> 8

55

Ala Ile Gly Glu Val Pro Gly Pro Met Val His Gly Ala Val Ser Phe
35 40 45

26/67

Val Thr Glu Ala Asp Ser Asp Asp Gly Leu Pro His Thr Leu Glu His
50 55 60

5
Leu Val Phe Met Gly Ser Lys Lys Tyr Pro Phe Lys Gly Val Leu Asp
65 70 75 80

10 Val Ile Ala Asn Arg Cys Leu Ala Asp Gly Thr Asn Ala Trp Thr Asp
85 90 95

15 Thr Asp His Thr Ala Tyr Thr Leu Ser Thr Val Gly Ser Asp Gly Phe
100 105 110

20 Leu Lys Val Leu Pro Val Tyr Ile Asn His Leu Leu Thr Pro Met Leu
115 120 125

Thr Ala Ser Gln Phe Ala Thr Glu Val His His Ile Thr Gly Glu Gly
130 135 140

25 Asn Asp Ala Gly Val Val Tyr Ser Glu Met Gln Asp His Glu Ser Glu
145 150 155 160

30 Met Glu Ser Ile Met Asp Arg Lys Thr Lys Glu Val Ile Tyr Pro Pro
165 170 175

35 Phe Asn Pro Tyr Ala Val Asp Thr Gly Gly Arg Leu Lys Asn Leu Arg
180 185 190

40 Glu Ser Cys Thr Leu Glu Lys Val Arg Asp Tyr His Lys Lys Phe Tyr
195 200 205

His Leu Ser Asn Met Val Val Thr Val Cys Gly Met Val Asp His Asp
210 215 220

45 Gln Val Leu Glu Ile Met Asn Asn Val Glu Asn Glu His Met Ser Thr
225 230 235 240

50 Val Pro Asp His Phe Pro Lys Pro Phe Ser Phe Ala Leu Ser Asp Ile
245 250 255

Lys Glu Ser Thr Val His Arg Val Glu Cys Pro Thr Asp Asp Ala Ser
260 265 270

55 Arg Gly Ala Val Glu Val Ala Trp Phe Ala His Ser Pro Ser Asp Leu
275 280 285

27/67

Glu Thr His Ser Ser Leu His Val Leu Phe Asp Tyr Leu Ser Asn Thr
 290 295 300

5

Ser Val Ala Pro Leu Gln Lys Asp Phe Ile Leu Leu Glu Asp Pro Leu
 305 310 315 320

10

Ala Ser Ser Val Ser Phe His Ile Ala Glu Gly Val Arg Cys Asp Leu
 325 330 335

15

Arg Leu Asn Phe Ala Gly Val Pro Val Glu Lys Leu Asp Glu Cys Ala
 340 345 350

20

Pro Lys Phe Phe Asp Lys Thr Val Arg Glu His Leu Glu Glu Ala Asn
 355 360 365

Phe Asp Met Glu Arg Met Gly Tyr Leu Ile Asp Gln Thr Ile Leu Asn
 370 375 380

25

Glu Leu Val Lys Leu Glu Thr Asn Ala Pro Lys Asp Ile Met Ser His
 385 390 395 400

30

Ile Ile Gly His Gln Leu Phe Asp Asn Glu Asp Glu Glu Leu Phe Lys
 405 410 415

35

Lys Arg Thr Asn Glu Ile Asp Phe Leu Lys Lys Leu Lys Ser Glu Pro
 420 425 430

40

Ala Ser Tyr Trp Val Gln Leu Val Asn Lys Tyr Phe Thr Ala Pro Ser
 435 440 445

Ala Thr Val Ile Gly Val Pro Asn Glu Glu Leu Val Asp Lys Ile Ala
 450 455 460

45

Glu Glu Glu Glu Lys Arg Ile Ala Ala Gln Cys Glu Lys Leu Gly Lys
 465 470 475 480

50

Lys Gly Leu Glu Glu Ala Gly Lys Ser Leu Glu Ala Ala Ile Leu Glu
 485 490 495

Asn Thr Ala Asn His Pro Ser Ala Glu Leu Leu Asp Gln Leu Ile Val
 500 505 510

55

Lys Asp Leu Glu Ala Phe Asp Arg Phe Pro Val Gln Ser Leu Thr Ser
 515 520 525

28/67

Asn Ser Pro Ser Leu Thr Pro Gln Gln Ser Thr Phe Leu Ala Gln Phe
 530 535 540

5 Pro Phe His Ala Asn Leu His Asn Cys Pro Thr Lys Phe Val Glu Ile
 545 550 555 560

10 Phe Phe Leu Leu Asp Ser Ser Asn Leu Ser Ile Glu Asp Arg Ser Tyr
 565 570 575

15 Leu Phe Leu Tyr Thr Asp Leu Leu Phe Glu Ser Pro Ala Met Ile Asp
 580 585 590

Gly Val Leu Thr Ser Ala Asp Asp Val Ala Lys His Phe Thr Lys Asp
 595 600 605

20 Leu Ile Asp His Ser Ile Gln Val Gly Val Ser Gly Leu Tyr Asp Arg
 610 615 620

25 Phe Val Asn Leu Arg Ile Lys Val Gly Ala Asp Lys Tyr Pro Leu Leu
 625 630 635 640

30 Ala Lys Trp Ala Gln Ile Phe Thr Gln Gly Val Val Phe Asp Pro Ser
 645 650 655

Arg Ile His Gln Cys Ala Gln Lys Leu Ala Gly Glu Ala Arg Asp Arg
 660 665 670

35 Lys Arg Asp Gly Cys Thr Val Ala Ser Thr Ala Val Ala Ser Met Val
 675 680 685

40 Tyr Gly Lys Asn Thr Asn Cys Ile Leu Phe Asp Glu Leu Val Leu Glu
 690 695 700

45 Lys Leu His Glu Lys Ile Ser Lys Asp Val Met Lys Asn Pro Glu Ala
 705 710 715 720

Val Leu Glu Lys Leu Glu Gln Val Arg Ser Ala Leu Phe Ser Asn Gly
 725 730 735

50 Val Asn Ala His Phe Val Ala Asp Val Asp Ser Ile Asp Pro Lys Met
 740 745 750

55 Leu Ser Ser Asp Leu Trp Thr Trp Val Gln Ala Asp Pro Arg Phe Gly
 755 760 765

Pro Gly His Gln Phe Ser Ala Glu Ala Gly Glu Asn Val Ser Leu Glu

29/67

770

775

780

Leu Gly Lys Glu Leu Leu Ile Gly Val Gly Gly Ser Glu Ser Ser Phe
 5 785 790 795 800

Ile Tyr Gln Thr Ser Phe Leu Asp Ala Asn Trp Asn Ser Glu Glu Leu
 10 805 810 815

Ile Pro Ala Met Ile Phe Gly Gln Tyr Leu Ser Gln Cys Glu Gly Pro
 820 825 830

Leu Trp Arg Ala Ile Arg Gly Asp Gly Leu Ala Tyr Gly Ala Asn Val
 835 840 845

Phe Val Lys Pro Asp Arg Lys Gln Ile Thr Leu Ser Leu Tyr Arg Cys
 20 850 855 860

Ala Gln Pro Ala Val Ala Tyr Glu Arg Thr Arg Asp Ile Ile Arg Lys
 25 865 870 875 880

Ile Val Glu Ser Gly Glu Ile Ser Lys Ala Glu Phe Glu Gly Ala Lys
 30 885 890 895

Arg Ser Thr Val Phe Glu Met Met Lys Arg Glu Gly Thr Val Ser Gly
 900 905 910

Ala Ala Lys Ile Ser Ile Leu Asn Asn Phe Arg Gln Thr Pro His Pro
 915 920 925
 Phe Asn Ile Asp Leu Cys Arg Arg Ile Trp Asn Leu Thr Ser Glu Glu
 930 935 940

Met Val Lys Ile Gly Gly Pro Pro Leu Ala Arg Leu Phe Asp Glu Lys
 945 950 955 960

Cys Phe Val Arg Ser Ile Ala Val His Pro Ser Lys Leu Asn Glu Met
 965 970 975

Lys Lys Ala Phe Pro Gly Ser Ser Lys Ile Lys Ile Ser Asp Leu Gln
 980 985 990

Phe Ala Cys
 55 995

<210> 9
 <211> 962

30/67

<212> PRT

<213> Escherichia coli

<400> 9

5

Met Pro Arg Ser Thr Trp Phe Lys Ala Leu Leu Leu Val Ala Leu
 1 5 10 15

10 Trp Ala Pro Leu Ser Gln Ala Glu Thr Gly Trp Gln Pro Ile Gln Glu
 20 25 30

15 Thr Ile Arg Lys Ser Asp Lys Asp Asn Arg Gln Tyr Gln Ala Ile Arg
 35 40 45

20 Leu Asp Asn Gly Met Val Val Leu Leu Val Ser Asp Pro Gln Ala Val
 50 55 60

Lys Ser Leu Ser Ala Leu Val Val Pro Val Gly Ser Leu Glu Asp Pro
 65 70 75 80

25

Glu Ala Tyr Gln Gly Leu Ala His Tyr Leu Glu His Met Ser Leu Met
 85 90 95

30 Gly Ser Lys Lys Tyr Pro Gln Ala Asp Ser Leu Ala Glu Tyr Leu Lys
 100 105 110

35 Met His Gly Gly Ser His Asn Ala Ser Thr Ala Pro Tyr Arg Thr Ala
 115 120 125

Phe Tyr Leu Glu Val Glu Asn Asp Ala Leu Pro Gly Ala Val Asp Arg
 130 135 140

40

Leu Ala Asp Ala Ile Ala Glu Pro Leu Leu Asp Lys Lys Tyr Ala Glu
 145 150 155 160

45 Arg Glu Arg Asn Ala Val Asn Ala Glu Leu Thr Met Ala Arg Thr Arg
 165 170 175

50 Asp Gly Met Arg Met Ala Gln Val Ser Ala Glu Thr Ile Asn Pro Ala
 180 185 190

His Pro Gly Ser Lys Phe Ser Gly Gly Asn Leu Glu Thr Leu Ser Asp
 195 200 205

55

Lys Pro Gly Asn Pro Val Gln Gln Ala Leu Lys Asp Phe His Glu Lys
 210 215 220

31/67

Tyr Tyr Ser Ala Asn Leu Met Lys Ala Val Ile Tyr Ser Asn Lys Pro
 225 230 235 240
 5
 Leu Pro Glu Leu Ala Lys Met Ala Ala Asp Thr Phe Gly Arg Val Pro
 245 250 255
 10 Asn Lys Glu Ser Lys Lys Pro Glu Ile Thr Val Pro Val Val Thr Asp
 260 265 270
 15 Ala Gln Lys Gly Ile Ile Ile His Tyr Val Pro Ala Leu Pro Arg Lys
 275 280 285
 20 Val Leu Arg Val Glu Phe Arg Ile Asp Asn Asn Ser Ala Lys Phe Arg
 290 295 300
 Ser Lys Thr Asp Glu Leu Ile Thr Tyr Leu Ile Gly Asn Arg Ser Pro
 305 310 315 320
 25 Gly Thr Leu Ser Asp Trp Leu Gln Lys Gln Gly Leu Val Glu Gly Ile
 325 330 335
 30 Ser Ala Asn Ser Asp Pro Ile Val Asn Gly Asn Ser Gly Val Leu Ala
 340 345 350
 35 Ile Ser Ala Ser Leu Thr Asp Lys Gly Leu Ala Asn Arg Asp Gln Val
 355 360 365
 Val Ala Ala Ile Phe Ser Tyr Leu Asn Leu Leu Arg Glu Lys Gly Ile
 370 375 380
 40 Asp Lys Gln Tyr Phe Asp Glu Leu Ala Asn Val Leu Asp Ile Asp Phe
 385 390 395 400
 45 Arg Tyr Pro Ser Ile Thr Arg Asp Met Asp Tyr Val Glu Trp Leu Ala
 405 410 415
 50 Asp Thr Met Ile Arg Val Pro Val Glu His Thr Leu Asp Ala Val Asn
 420 425 430
 Ile Ala Asp Arg Tyr Asp Ala Lys Ala Val Lys Glu Arg Leu Ala Met
 435 440 445
 55 Met Thr Pro Gln Asn Ala Arg Ile Trp Tyr Ile Ser Pro Lys Glu Pro
 450 455 460

32/67

His Asn Lys Thr Ala Tyr Phe Val Asp Ala Pro Tyr Gln Val Asp Lys
 465 470 475 480

5 Ile Ser Ala Gln Thr Phe Ala Asp Trp Gln Lys Lys Ala Ala Asp Ile
 485 490 495

10 Ala Leu Ser Leu Pro Glu Leu Asn Pro Tyr Ile Pro Asp Asp Phe Ser
 500 505 510

15 Leu Ile Lys Ser Glu Lys Lys Tyr Asp His Pro Glu Leu Ile Val Asp
 515 520 525

Glu Ser Asn Leu Arg Val Val Tyr Ala Pro Ser Arg Tyr Phe Ala Ser
 530 535 540

20 Glu Pro Lys Ala Asp Val Ser Leu Ile Leu Arg Asn Pro Lys Ala Met
 545 550 555 560

25 Asp Ser Ala Arg Asn Gln Val Met Phe Ala Leu Asn Asp Tyr Leu Ala
 565 570 575

30 Gly Leu Ala Leu Asp Gln Leu Ser Asn Gln Ala Ser Val Gly Gly Ile
 580 585 590

35 Ser Phe Ser Thr Asn Ala Asn Asn Gly Leu Met Val Asn Ala Asn Gly
 595 600 605
 Tyr Thr Gln Arg Leu Pro Gln Leu Phe Gln Ala Leu Leu Glu Gly Tyr
 610 615 620

40 Phe Ser Tyr Thr Ala Thr Glu Asp Gln Leu Glu Gln Ala Lys Ser Trp
 625 630 635 640

45 Tyr Asn Gln Met Met Asp Ser Ala Glu Lys Gly Lys Ala Phe Glu Gln
 645 650 655

Ala Ile Met Pro Ala Gln Met Leu Ser Gln Val Pro Tyr Phe Ser Arg
 660 665 670

50 Asp Glu Arg Arg Lys Ile Leu Pro Ser Ile Thr Leu Lys Glu Val Leu
 675 680 685

55 Ala Tyr Arg Asp Ala Leu Lys Ser Gly Ala Arg Pro Glu Phe Met Val
 690 695 700

Ile Gly Asn Met Thr Glu Ala Gln Ala Thr Thr Leu Ala Arg Asp Val

33/67

705		710		715		720
5	Gln Lys Gln Leu Gly Ala Asp Gly Ser Glu Trp Cys Arg Asn Lys Asp	725		730		735
10	Val Val Val Asp Lys Lys Gln Ser Val Ile Phe Glu Lys Ala Gly Asn	740		745		750
15	Ser Thr Asp Ser Ala Leu Ala Val Phe Val Pro Thr Gly Tyr Asp	755		760		765
20	Glu Tyr Thr Ser Ser Ala Tyr Ser Ser Leu Leu Gly Gln Ile Val Gln	770		775		780
25	Pro Trp Phe Tyr Asn Gln Leu Arg Thr Glu Glu Gln Leu Gly Tyr Ala	785		790		795
30	Val Phe Ala Phe Pro Met Ser Val Gly Arg Gln Trp Gly Met Gly Phe	805		810		815
35	Leu Leu Gln Ser Asn Asp Lys Gln Pro Ser Phe Leu Trp Glu Arg Tyr	820		825		830
40	Lys Ala Phe Phe Pro Thr Ala Glu Ala Lys Leu Arg Ala Met Lys Pro	835		840		845
45	Asp Glu Phe Ala Gln Ile Gln Gln Ala Val Ile Thr Gln Met Leu Gln	850		855		860
50	Ala Pro Gln Thr Leu Gly Glu Glu Ala Ser Lys Leu Ser Lys Asp Phe	865		870		875
55	Asp Arg Gly Asn Met Arg Phe Asp Ser Arg Asp Lys Ile Val Ala Gln	885		890		895
60	Ile Lys Leu Leu Thr Pro Gln Lys Leu Ala Asp Phe Phe His Gln Ala	900		905		910
65	Val Val Glu Pro Gln Gly Met Ala Ile Leu Ser Gln Ile Ser Gly Ser	915		920		925
70	Gln Asn Gly Lys Ala Glu Tyr Val His Pro Glu Gly Trp Lys Val Trp	930		935		940
75	Glu Asn Val Ser Ala Leu Gln Gln Thr Met Pro Leu Met Ser Glu Lys	945		950		955
80						960

34/67

Asn Glu

5

<210> 10
 <211> 1161
 <212> PRT
 10 <213> Homo sapiens

<400> 10

Met Leu Arg Arg Val Ala Val Ala Ala Val Phe Ala Thr Gly Arg Lys
 15 1 5 10 15

Leu Arg Cys Glu Ala Gly Arg Asp Val Thr Ala Val Gly Arg Ile Glu
 20 20 25 30

Ala Arg Gly Leu Cys Glu Glu Ser Ala Lys Pro Phe Pro Thr Leu Thr
 35 40 45

25 Met Pro Gly Arg Asn Lys Ala Lys Ser Thr Cys Ser Cys Pro Asp Leu
 50 55 60

30 Gln Pro Asn Gly Gln Asp Leu Gly Glu Ser Gly Arg Val Ala Arg Leu
 65 70 75 80
 Gly Ala Asp Glu Ser Glu Glu Glu Gly Arg Ser Leu Ser Asn Val Gly
 85 90 95

35 Asp Pro Glu Ile Ile Lys Ser Pro Ser Asp Pro Lys Gln Tyr Arg Tyr
 100 105 110

40 Ile Lys Leu Gln Asn Gly Leu Gln Ala Leu Leu Ile Ser Asp Leu Ser
 115 120 125

45 Asn Val Glu Gly Lys Thr Gly Asn Ala Thr Asp Glu Glu Glu Glu Glu
 130 135 140

Glu Glu Glu Glu Glu Glu Gly Glu Glu Glu Glu Glu Glu Glu Asp
 145 150 155 160

50 Asp Asp Asp Asp Asp Asp Glu Asp Ser Gly Ala Glu Ile Gln Asp Asp
 165 170 175

55 Asp Glu Glu Gly Phe Asp Asp Glu Glu Glu Phe Asp Asp Asp Glu His
 180 185 190

35/67

Asp Asp Asp Asp Leu Asp Asn Glu Glu Asn Glu Leu Glu Glu Leu Glu
 195 200 205

5 Glu Arg Val Glu Ala Arg Lys Lys Thr Thr Glu Lys Gln Ser Ala Ala
 210 215 220

10 Ala Leu Cys Val Gly Val Gly Ser Phe Ala Asp Pro Asp Asp Leu Pro
 225 230 235 240

Gly Leu Ala His Phe Leu Glu His Met Val Phe Met Gly Ser Leu Lys
 245 250 255

15 Tyr Pro Asp Glu Asn Gly Phe Asp Ala Phe Leu Lys Lys His Gly Gly
 260 265 270

20 Ser Asp Asn Ala Ser Thr Asp Cys Glu Arg Thr Val Phe Gln Phe Asp
 275 280 285

25 Val Gln Arg Lys Tyr Phe Lys Glu Ala Leu Asp Arg Trp Ala Gln Phe
 290 295 300

30 Phe Ile His Pro Leu Met Ile Arg Asp Ala Ile Asp Arg Glu Val Glu
 305 310 315 320
 Ala Val Asp Ser Glu Tyr Gln Leu Ala Arg Pro Ser Asp Ala Asn Arg
 325 330 335

35 Lys Glu Met Leu Phe Gly Ser Leu Ala Arg Pro Gly His Pro Met Gly
 340 345 350

40 Lys Phe Phe Trp Gly Asn Ala Glu Thr Leu Lys His Glu Pro Lys Lys
 355 360 365

45 Asn Asn Ile Asp Thr His Ala Arg Leu Arg Glu Phe Trp Met Arg Tyr
 370 375 380

Tyr Ser Ala His Tyr Met Thr Leu Val Val Gln Ser Lys Glu Thr Leu
 385 390 395 400

50 Asp Thr Leu Glu Lys Trp Val Thr Glu Ile Phe Ser Gln Ile Pro Asn
 405 410 415

55 Asn Gly Leu Pro Lys Pro Asn Phe Ser His Leu Thr Asp Pro Phe Asp
 420 425 430

Thr Pro Ala Phe Asn Lys Leu Tyr Arg Val Val Pro Ile Arg Lys Ile

36/67

	435		440		445
5	His Ala Leu Thr Ile Thr Trp Ala Leu Pro Pro Gln Gln Gln His Tyr				
	450		455		460
10	Arg Val Lys Pro Leu His Tyr Ile Ser Trp Leu Val Gly His Glu Gly				
	465		470		475 480
15	Lys Gly Ser Ile Leu Ser Tyr Leu Arg Lys Lys Cys Trp Ala Leu Ala				
			485		490 495
20	Leu Phe Gly Gly Asn Gly Glu Thr Gly Phe Glu Gln Asn Ser Thr Tyr				
			500		505 510
25	Ser Val Phe Ser Ile Ser Ile Thr Leu Thr Asp Glu Gly Tyr Glu His				
			515		520 525
30	Phe Tyr Glu Val Ala His Thr Val Phe Gln Tyr Leu Lys Met Leu Gln				
			530		535 540
35	Lys Leu Gly Pro Glu Lys Arg Val Phe Glu Glu Ile Gln Lys Ile Glu				
			545		550 555 560
40	Asp Asn Glu Phe His Tyr Gln Glu Gln Thr Asp Pro Val Glu Tyr Val				
			565		570 575
45	Glu Asn Met Cys Glu Asn Met Gln Leu Tyr Pro Arg Gln Asp Phe Leu				
			580		585 590
50	Thr Gly Asp Gln Leu Leu Phe Glu Tyr Lys Pro Glu Val Ile Ala Glu				
			595		600 605
55	Ala Leu Asn Gln Leu Val Pro Gln Lys Ala Asn Leu Val Leu Leu Ser				
			610		615 620
60	Gly Ala Asn Glu Gly Arg Cys Asp Leu Lys Glu Lys Trp Phe Gly Thr				
			625		630 635 640
65	Gln Tyr Ser Ile Glu Asp Ile Glu Asn Ser Trp Thr Glu Leu Trp Lys				
			645		650 655
70	Ser Asn Phe Asp Leu Asn Ser Asp Leu His Leu Pro Ala Glu Asn Lys				
			660		665 670
75	Tyr Ile Ala Thr Asp Phe Thr Leu Lys Ala Phe Asp Cys Pro Glu Thr				
			675		680 685

5	Glu Tyr Pro Ala Lys Ile Val	690	695	700	Gly Cys Leu Trp Tyr
10	Lys Lys Asp Asn Lys Phe Lys Ile Pro Lys Ala Tyr Ile Arg Phe His	705	710	715	720
15	Leu Ile Ser Pro Leu Ile Gln Lys Ser Ala Ala Asn Val Val Leu Phe	725	730	735	
20	Asp Ile Phe Val Asn Ile Leu Thr His Asn Leu Ala Glu Pro Ala Tyr	740	745	750	
25	Glu Ala Asp Val Ala Gln Leu Glu Tyr Lys Leu Val Ala Gly Glu His	755	760	765	
30	Gly Leu Ile Ile Arg Val Lys Gly Phe Asn His Lys Leu Pro Leu Leu	770	775	780	
35	Phe Gln Leu Ile Ile Asp Tyr Leu Thr Glu Phe Ser Ser Thr Pro Ala	785	790	795	800
40	Val Phe Thr Met Ile Thr Glu Gln Leu Lys Lys Thr Tyr Phe Asn Ile	805	810	815	
45	Leu Ile Lys Pro Glu Thr Leu Ala Lys Asp Val Arg Leu Leu Ile Leu	820	825	830	
50	Glu Tyr Ser Arg Trp Ser Met Ile Asp Lys Tyr Arg Ala Leu Met Asp	835	840	845	
55	Gly Leu Ser Leu Glu Ser Leu Leu Asn Phe Val Lys Asp Phe Lys Ser	850	855	860	
60	Gln Leu Phe Val Glu Gly Leu Val Gln Gly Asn Val Thr Ser Thr Glu	865	870	875	880
65	Ser Met Asp Phe Leu Arg Tyr Val Val Asp Lys Leu Asn Phe Val Pro	885	890	895	
70	Leu Glu Arg Glu Met Pro Val Gln Phe Gln Val Val Glu Leu Pro Ser	900	905	910	
75	Gly His His Leu Cys Lys Val Arg Ala Leu Asn Lys Gly Asp Ala Asn	915	920	925	

38/67

Ser Glu Val Thr Val Tyr Tyr Gln Ser Gly Thr Arg Ser Leu Arg Glu
 930 935 940

5

Tyr Thr Leu Met Glu Leu Leu Val Met His Met Glu Glu Pro Cys Phe
 945 950 955 960

10 Asp Phe Leu Arg Thr Lys Gln Thr Leu Gly Tyr His Val Tyr Pro Thr
 965 970 975

15 Cys Arg Asn Thr Ser Gly Ile Leu Gly Phe Ser Val Thr Val Gly Thr
 980 985 990

20 Gln Ala Thr Lys Tyr Asn Ser Glu Thr Val Asp Lys Lys Ile Glu Glu
 995 1000 1005

Phe Leu Ser Ser Phe Glu Glu Lys Ile Glu Asn Leu Thr Glu Asp
 1010 1015 1020

25 Ala Phe Asn Thr Gln Val Thr Ala Leu Ile Lys Leu Lys Glu Cys
 1025 1030 1035
 Glu Asp Thr His Leu Gly Glu Glu Val Asp Arg Asn Trp Asn Glu
 1040 1045 1050

30 Val Val Thr Gln Gln Tyr Leu Phe Asp Arg Leu Ala His Glu Ile
 1055 1060 1065

35 Glu Ala Leu Lys Ser Phe Ser Lys Ser Asp Leu Val Ser Trp Phe
 1070 1075 1080

40 Lys Ala His Arg Gly Pro Gly Ser Lys Met Leu Ser Val His Val
 1085 1090 1095

45 Val Gly Tyr Gly Lys Tyr Glu Leu Glu Glu Asp Gly Ala Pro Val
 1100 1105 1110

50 Cys Glu Asp Pro Asn Ser Arg Glu Gly Met Gln Leu Ile Tyr Leu
 1115 1120 1125

Pro Pro Ser Pro Leu Leu Ala Glu Ser Thr Thr Pro Ile Thr Asp
 1130 1135 1140

55 Ile Arg Ala Phe Thr Ala Thr Leu Ser Leu Phe Pro Tyr His Lys
 1145 1150 1155

39/67

Ile Val Lys
1160

5 <210> 11
 <211> 1019
 <212> PRT
 <213> Homo sapiens

10 <400> 11

Met Arg Tyr Arg Leu Ala Trp Leu Leu His Pro Ala Leu Pro Ser Thr
 1 5 10 15

15

Phe Arg Ser Val Leu Gly Ala Arg Leu Pro Pro Pro Glu Arg Leu Cys
 20 25 30

20 Gly Phe Gln Lys Lys Thr Tyr Ser Lys Met Asn Asn Pro Ala Ile Lys
 35 40 45

Arg Ile Gly Asn His Ile Thr Lys Ser Pro Glu Asp Lys Arg Glu Tyr
 25 50 55 60
 Arg Gly Leu Glu Leu Ala Asn Gly Ile Lys Val Leu Leu Met Ser Asp
 65 70 75 80

30 Pro Thr Thr Asp Lys Ser Ser Ala Ala Leu Asp Val His Ile Gly Ser
 85 90 95

35 Leu Ser Asp Pro Pro Asn Ile Ala Gly Leu Ser His Phe Cys Glu His
 100 105 110

Met Leu Phe Leu Gly Thr Lys Lys Tyr Pro Lys Glu Asn Glu Tyr Ser
 115 120 125

40 Gln Phe Leu Ser Glu His Ala Gly Ser Ser Asn Ala Phe Thr Ser Gly
 130 135 140

45

Glu His Thr Asn Tyr Tyr Phe Asp Val Ser His Glu His Leu Glu Gly
 145 150 155 160

50 Ala Leu Asp Arg Phe Ala Gln Phe Phe Leu Cys Pro Leu Phe Asp Glu
 165 170 175

55 Ser Cys Lys Asp Arg Glu Val Asn Ala Val Asp Ser Glu His Glu Lys
 180 185 190

Asn Val Met Asn Asp Ala Trp Arg Leu Phe Gln Leu Glu Lys Ala Thr
 195 200 205

40/67

Gly Asn Pro Lys His Pro Phe Ser Lys Phe Gly Thr Gly Asn Lys Tyr
 210 215 220
 5

Thr Leu Glu Thr Arg Pro Asn Gln Glu Gly Ile Asp Val Arg Gln Glu
 225 230 235 240

10

Leu Leu Lys Phe His Ser Ala Tyr Tyr Ser Ser Asn Leu Met Ala Val
 245 250 255

15 Cys Val Leu Gly Arg Glu Ser Leu Asp Asp Leu Thr Asn Leu Val Val
 260 265 270

20 Lys Leu Phe Ser Glu Val Glu Asn Lys Asn Val Pro Leu Pro Glu Phe
 275 280 285

Pro Glu His Pro Phe Gln Glu Glu His Leu Lys Gln Leu Tyr Lys Ile
 290 295 300

25 Val Pro Ile Lys Asp Ile Arg Asn Leu Tyr Val Thr Phe Pro Ile Pro
 305 310 315 320

30 Asp Leu Gln Lys Tyr Tyr Lys Ser Asn Pro Gly His Tyr Leu Gly His
 325 330 335

Leu Ile Gly His Glu Gly Pro Gly Ser Leu Leu Ser Glu Leu Lys Ser
 340 345 350

35

Lys Gly Trp Val Asn Thr Leu Val Gly Gly Gln Lys Glu Gly Ala Arg
 355 360 365

40

Gly Phe Met Phe Phe Ile Ile Asn Val Asp Leu Thr Glu Glu Gly Leu
 370 375 380

45 Leu His Val Glu Asp Ile Ile Leu His Met Phe Gln Tyr Ile Gln Lys
 385 390 395 400

Leu Arg Ala Glu Gly Pro Gln Glu Trp Val Phe Gln Glu Cys Lys Asp
 405 410 415

50

Leu Asn Ala Val Ala Phe Arg Phe Lys Asp Lys Glu Arg Pro Arg Gly
 420 425 430

55

Tyr Thr Ser Lys Ile Ala Gly Ile Leu His Tyr Tyr Pro Leu Glu Glu
 435 440 445

41/67

Val Leu Thr Ala Glu Tyr Leu Leu Glu Glu Phe Arg Pro Asp Leu Ile
450 455 460

5
Glu Met Val Leu Asp Lys Leu Arg Pro Glu Asn Val Arg Val Ala Ile
465 470 475 480

10 Val Ser Lys Ser Phe Glu Gly Lys Thr Asp Arg Thr Glu Glu Trp Tyr
485 490 495

15 Gly Thr Gln Tyr Lys Gln Glu Ala Ile Pro Asp Glu Val Ile Lys Lys
500 505 510

20 Trp Gln Asn Ala Asp Leu Asn Gly Lys Phe Lys Leu Pro Thr Lys Asn
515 520 525

Glu Phe Ile Pro Thr Asn Phe Glu Ile Leu Pro Leu Glu Lys Glu Ala
530 535 540

25 Thr Pro Tyr Pro Ala Leu Ile Lys Asp Thr Val Met Ser Lys Leu Trp
545 550 555 560

30 Phe Lys Gln Asp Asp Lys Lys Lys Lys Pro Lys Ala Cys Leu Asn Phe
565 570 575

Glu Phe Phe Ser Pro Phe Ala Tyr Val Asp Pro Leu His Cys Asn Met
580 585 590

35
Ala Tyr Leu Tyr Leu Glu Leu Leu Lys Asp Ser Leu Asn Glu Tyr Ala
595 600 605

40 Tyr Ala Ala Glu Leu Ala Gly Leu Ser Tyr Asp Leu Gln Asn Thr Ile
610 615 620

45 Tyr Gly Met Tyr Leu Ser Val Lys Gly Tyr Asn Asp Lys Gln Pro Ile
625 630 635 640

50 Leu Leu Lys Lys Ile Ile Glu Lys Met Ala Thr Phe Glu Ile Asp Glu
645 650 655

Lys Arg Phe Glu Ile Ile Lys Glu Ala Tyr Met Arg Ser Leu Asn Asn
660 665 670

55
Phe Arg Ala Glu Gln Pro His Gln His Ala Met Tyr Tyr Leu Arg Leu
675 680 685

42/67

Leu Met Thr Glu Val Ala Trp Thr Lys Asp Glu Leu Lys Glu Ala Leu
 690 695 700

5 Asp Asp Val Thr Leu Pro Arg Leu Lys Ala Phe Ile Pro Gln Leu Leu
 705 710 715 720

10 Ser Arg Leu His Ile Glu Ala Leu Leu His Gly Asn Ile Thr Lys Gln
 725 730 735

15 Ala Ala Leu Gly Ile Met Gln Met Val Glu Asp Thr Leu Ile Glu His
 740 745 750

20 Ala His Thr Lys Pro Leu Leu Pro Ser Gln Leu Val Arg Tyr Arg Glu
 755 760 765

Val Gln Leu Pro Asp Arg Gly Trp Phe Val Tyr Gln Gln Arg Asn Glu
 770 775 780

Val His Asn Asn Cys Gly Ile Glu Ile Tyr Tyr Gln Thr Asp Met Gln
 785 790 795 800

25 Ser Thr Ser Glu Asn Met Phe Leu Glu Leu Phe Cys Gln Ile Ile Ser
 805 810 815

30 Glu Pro Cys Phe Asn Thr Leu Arg Thr Lys Glu Gln Leu Gly Tyr Ile
 820 825 830

35 Val Phe Ser Gly Pro Arg Arg Ala Asn Gly Ile Gln Ser Leu Arg Phe
 835 840 845

40 Ile Ile Gln Ser Glu Lys Pro Pro His Tyr Leu Glu Ser Arg Val Glu
 850 855 860

45 Ala Phe Leu Ile Thr Met Glu Lys Ser Ile Glu Asp Met Thr Glu Glu
 865 870 875 880

Ala Phe Gln Lys His Ile Gln Ala Leu Ala Ile Arg Arg Leu Asp Lys
 885 890 895

50 Pro Lys Lys Leu Ser Ala Glu Cys Ala Lys Tyr Trp Gly Glu Ile Ile
 900 905 910

55 Ser Gln Gln Tyr Asn Phe Asp Arg Asp Asn Thr Glu Val Ala Tyr Leu
 915 920 925

Lys Thr Leu Thr Lys Glu Asp Ile Ile Lys Phe Tyr Lys Glu Met Leu

43/67

930

935

940

Ala Val Asp Ala Pro Arg Arg His Lys Val Ser Val His Val Leu Ala
 5 945 950 955 960

Arg Glu Met Asp Ser Cys Pro Val Val Gly Glu Phe Pro Cys Gln Asn
 10 965 970 975

Asp Ile Asn Leu Ser Gln Ala Pro Ala Leu Pro Gln Pro Glu Val Ile
 980 985 990

15 Gln Asn Met Thr Glu Phe Lys Arg Gly Leu Pro Leu Phe Pro Leu Val
 995 1000 1005

20 Lys Pro His Ile Asn Phe Met Ala Ala Lys Leu
 1010 1015

<210> 12

<211> 1265

<212> PRT

25 <213> Arabidopsis thaliana

<400> 12

Met Ala Ser Ser Ser Ser Ser Ile Phe Thr Gly Val Lys Phe Ser Pro
 30 1 5 10 15

Ile Leu Ala Pro Phe Asn Ser Gly Asp Ser Arg Arg Ser Arg Tyr Leu
 35 20 25 30

Lys Asp Ser Arg Asn Lys Val Arg Phe Asn Pro Ser Ser Pro Arg Leu
 35 40 45

40 Thr Pro His Arg Val Arg Val Glu Ala Pro Ser Leu Ile Pro Tyr Asn
 50 55 60

45 Gly Leu Trp Ala Ala Gln Pro Asn Ser His Lys Gly Arg Leu Lys Arg
 65 70 75 80

50 Asn Ile Val Ser Gly Lys Glu Ala Thr Gly Ile Ser Leu Ser Gln Gly
 85 90 95

Arg Asn Phe Cys Leu Thr Cys Lys Arg Asn Gln Ala Gly Ile Arg Arg
 55 100 105 110

Ala Leu Pro Ser Ala Phe Val Asp Arg Thr Ala Phe Ser Leu Ser Arg
 115 120 125

44/67

Ser Ser Leu Thr Ser Ser Leu Arg Lys His Ser Gln Ile Val Asn Ala
130 135 140

5 Thr Leu Gly Pro Asp Glu Pro His Ala Ala Gly Thr Ala Trp Pro Asp
145 150 155 160

10 Gly Ile Val Ala Glu Arg Gln Asp Leu Asp Leu Leu Pro Pro Glu Ile
165 170 175

15 Asp Ser Ala Glu Leu Glu Ala Phe Leu Gly Cys Glu Leu Pro Ser His
180 185 190

20 Pro Lys Leu His Arg Gly Gln Leu Lys Asn Gly Leu Arg Tyr Leu Ile
195 200 205

Leu Pro Asn Lys Val Pro Pro Asn Arg Phe Glu Ala His Met Glu Val
210 215 220

25 His Val Gly Ser Ile Asp Glu Glu Glu Asp Glu Gln Gly Ile Ala His
225 230 235 240

30 Met Ile Glu His Val Ala Phe Leu Gly Ser Lys Lys Arg Glu Lys Leu
245 250 255

35 Leu Gly Thr Gly Ala Arg Ser Asn Ala Tyr Thr Asp Phe His His Thr
260 265 270

40 Val Phe His Ile His Ser Pro Thr His Thr Lys Asp Ser Glu Asp Asp
275 280 285

45 Lys Phe Leu Ser Ser Arg Val Glu Lys Glu Arg Arg Ala Ile Leu Ser
305 310 315 320

50 Glu Leu Gln Met Met Asn Thr Ile Glu Tyr Arg Val Asp Cys Gln Leu
325 330 335

55 Leu Gln His Leu His Ser Glu Asn Lys Leu Gly Arg Arg Phe Pro Ile
340 345 350

Gly Leu Glu Glu Gln Ile Lys Lys Trp Asp Val Asp Lys Ile Arg Lys
355 360 365

45/67

Phe His Glu Arg Trp Tyr Phe Pro Ala Asn Ala Thr Leu Tyr Ile Val
 370 375 380

5

Gly Asp Ile Asp Asn Ile Pro Arg Ile Val His Asn Ile Glu Ala Val
 385 390 395 400

10 Phe Gly Lys Asn Gly Leu Asp Asn Glu Ser Thr Pro Ser Ser Pro Ser
 405 410 415

15 Pro Gly Ala Phe Gly Ala Met Ala Asn Phe Leu Val Pro Lys Leu Pro
 420 425 430

Ala Gly Leu Gly Gly Thr Phe Ser Asn Glu Lys Thr Asn Thr Ala Asp
 435 440 445

20 Gln Ser Lys Met Ile Lys Arg Glu Arg His Ala Ile Arg Pro Pro Val
 450 455 460

Glu His Asn Trp Ser Leu Pro Gly Thr Ser Val Asp Leu Lys Pro Pro
 25 465 470 475 480

Gln Ile Phe Lys His Glu Leu Leu Gln Asn Phe Ala Ile Asn Met Phe
 485 490 495

30

Cys Lys Ile Pro Val Ser Lys Val Gln Thr Phe Gly Asp Leu Arg Asn
 500 505 510

35

Val Leu Met Lys Arg Ile Phe Leu Ser Ala Leu His Phe Arg Ile Asn
 515 520 525

40 Thr Arg Tyr Lys Ser Ser Asn Pro Pro Phe Thr Ser Val Glu Leu Asp
 530 535 540

His Ser Asp Ser Gly Arg Glu Gly Cys Thr Val Thr Thr Leu Thr Val
 45 545 550 555 560

Thr Ala Glu Pro Gln Asn Trp Gln Asn Ala Val Lys Val Ala Val Gln
 565 570 575

50

Glu Val Arg Arg Leu Lys Glu Phe Gly Val Thr Arg Gly Glu Leu Thr
 580 585 590

55

Arg Tyr Met Asp Ala Leu Leu Lys Asp Ser Glu His Leu Ala Ala Met
 595 600 605

46/67

Ile Asp Asn Val Ser Ser Val Asp Asn Leu Asp Phe Ile Met Glu Ser
610 615 620

5 Asp Ala Leu Ser His Thr Val Met Asp Gln Thr Gln Gly His Glu Thr
625 630 635 640

10 Leu Val Ala Val Ala Gly Thr Val Thr Leu Glu Glu Val Asn Thr Val
645 650 655

15 Gly Ala Lys Val Leu Glu Phe Ile Ser Asp Phe Gly Arg Pro Thr Ala
660 665 670

20 Leu Leu Pro Ala Ala Ile Val Ala Cys Val Pro Thr Lys Val His Val
675 680 685
Asp Gly Val Gly Glu Ser Asp Phe Asn Ile Ser Pro Asp Glu Ile Ile
690 695 700

25 Glu Ser Val Lys Ser Gly Leu Leu Ala Pro Ile Glu Ala Glu Pro Glu
705 710 715 720

30 Leu Glu Val Pro Lys Glu Leu Ile Ser Gln Ser Gln Leu Lys Glu Leu
725 730 735

35 Thr Leu Gln Arg Asn Pro Cys Phe Val Pro Ile Pro Gly Ser Gly Leu
740 745 750

40 Asn Gly Ile Ala Val Asn Tyr Lys Lys Ser Thr Thr Glu Ser Arg Ala
770 775 780

45 Gly Val Met Arg Leu Ile Val Gly Gly Gly Arg Ala Ala Glu Thr Ser
785 790 795 800

50 Asp Ser Lys Gly Ala Val Val Val Gly Val Arg Thr Leu Ser Glu Gly
805 810 815

55 Asn His Leu Ile Asn Cys Ser Leu Glu Ser Thr Glu Glu Phe Ile Ala
835 840 845

Met Glu Phe Arg Phe Thr Leu Arg Asp Asn Gly Met Gln Ala Ala Phe

47/67

	850		855		860
5	Gln Leu Leu His Met Val	Leu Glu Arg Ser Val	Trp Leu Glu Asp Ala		
	865	870	875	880	
10	Phe Asp Arg Ala Arg Gln Leu Tyr Leu Ser Tyr Phe Arg Ser Ile Pro				
		885	890	895	
15	Lys Ser Leu Glu Arg Ala Thr Ala His Lys Leu Met Ile Ala Met Leu				
		900	905	910	
20	Asn Gly Asp Glu Arg Phe Val Glu Pro Thr Pro Lys Ser Leu Gln Ser				
		915	920	925	
	Leu Asn Leu Glu Ser Val Lys Asp Ala Val Met Ser His Phe Val Gly				
		930	935	940	
25	Asp Asn Met Glu Val Ser Ile Val Gly Asp Phe Ser Glu Glu Glu Ile				
		945	950	955	960
30	Glu Arg Cys Ile Leu Asp Tyr Leu Gly Thr Val Lys Ala Ser His Asp				
		965	970	975	
35	Ser Ala Lys Pro Pro Gly Ser Glu Pro Ile Leu Phe Arg Gln Pro Thr				
		980	985	990	
40	Ala Gly Leu Gln Phe Gln Gln Val Phe Leu Lys Asp Thr Asp Glu Arg				
		995	1000	1005	
45	Ala Cys Ala Tyr Ile Ala Gly Pro Ala Pro Asn Arg Trp Gly Phe				
		1010	1015	1020	
50	Thr Val Asp Gly Asp Asp Leu Phe Gln Ser Val Ser Lys Leu Pro				
		1025	1030	1035	
55	Val Ala His Asp Gly Leu Leu Lys Ser Glu Glu Gln Leu Leu Glu				
		1040	1045	1050	
60	Gly Gly Asp Arg Glu Leu Gln Lys Lys Leu Arg Ala His Pro Leu				
		1055	1060	1065	
65	Phe Phe Gly Val Thr Met Gly Leu Leu Ala Glu Ile Ile Asn Ser				
		1070	1075	1080	
70	Arg Leu Phe Thr Thr Val Arg Asp Ser Leu Gly Leu Thr Tyr Asp				
		1085	1090	1095	

48/67

5 Val Ser Phe Glu Leu Asn Leu Phe Asp Arg Leu Lys Leu Gly Trp
 1100 1105 1110
 Tyr Val Ile Ser Val Thr Ser Thr Pro Gly Lys Val Tyr Lys Ala
 1115 1120 1125
 10 Val Asp Ala Cys Lys Asn Val Leu Arg Gly Leu His Ser Asn Gln
 1130 1135 1140
 15 Ile Ala Pro Arg Glu Leu Asp Arg Ala Lys Arg Thr Leu Leu Met
 1145 1150 1155
 Arg His Glu Ala Glu Leu Lys Ser Asn Ala Tyr Trp Leu Asn Leu
 1160 1165 1170
 20 Leu Ala His Leu Gln Ala Ser Ser Val Gln Arg Lys Glu Leu Ser
 1175 1180 1185
 25 Cys Ile Lys Glu Leu Val Ser Leu Tyr Glu Ala Ala Ser Ile Glu
 1190 1195 1200
 30 Asp Ile Tyr Leu Ala Tyr Asn Gln Leu Arg Val Asp Glu Asp Ser
 1205 1210 1215
 35 Leu Tyr Ser Cys Ile Gly Ile Ala Gly Ala Gln Ala Gly Glu Glu
 1220 1225 1230
 Ile Thr Val Leu Ser Glu Glu Glu Glu Pro Glu Asp Val Phe Ser
 1235 1240 1245
 40 Gly Val Val Pro Val Gly Arg Gly Ser Ser Met Thr Thr Arg Pro
 1250 1255 1260
 45 Thr Thr
 1265
 <210> 13
 50 <211> 534
 <212> PRT
 <213> Homo sapiens
 <400> 13
 55 Met Arg Pro Asp Asp Lys Tyr His Glu Lys Gln Ala Gln Val Glu Ala
 1 5 10 15

49/67

Thr Lys Leu Lys Gln Lys Val Glu Ala Leu Ser Pro Gly Asp Arg Gln
20 25 30

5 Gln Ile Tyr Glu Lys Gly Leu Glu Leu Arg Ser Gln Gln Ser Lys Pro
35 40 45

10 Gln Asp Ala Ser Cys Leu Pro Ala Leu Lys Val Ser Asp Ile Glu Pro
50 55 60

15 Thr Ile Pro Val Thr Glu Leu Asp Val Val Leu Thr Ala Gly Asp Ile
65 70 75 80

Pro Val Gln Tyr Cys Ala Gln Pro Thr Asn Gly Met Val Tyr Phe Arg
85 90 95

20 Ala Phe Ser Ser Leu Asn Thr Leu Pro Glu Glu Leu Arg Pro Tyr Val
100 105 110

25 Pro Leu Phe Cys Ser Val Leu Thr Lys Leu Gly Cys Gly Leu Leu Asp
115 120 125

30 Tyr Arg Glu Gln Ala Gln Gln Ile Glu Leu Lys Thr Gly Gly Met Ser
130 135 140

Ala Ser Pro His Val Leu Pro Asp Asp Ser His Met Asp Thr Tyr Glu
145 150 155 160

35 Gln Gly Val Leu Phe Ser Ser Leu Cys Leu Asp Arg Asn Leu Pro Asp
165 170 175

40 Met Met Gln Leu Trp Ser Glu Ile Phe Asn Asn Pro Cys Phe Glu Glu
180 185 190

45 Glu Glu His Phe Lys Val Leu Val Lys Met Thr Ala Gln Glu Leu Ala
195 200 205

50 Asn Gly Ile Pro Asp Ser Gly His Leu Tyr Ala Ser Ile Arg Ala Gly
210 215 220

Arg Thr Leu Thr Pro Ala Gly Asp Leu Gln Glu Thr Phe Ser Gly Met
225 230 235 240

55 Asp Gln Val Arg Leu Met Lys Arg Ile Ala Glu Met Thr Asp Ile Lys
245 250 255

50/67

Pro Ile Leu Arg Lys Leu Pro Arg Ile Lys Lys His Leu Leu Asn Gly
 260 265 270

5 Asp Asn Met Arg Cys Ser Val Asn Ala Thr Pro Gln Gln Met Pro Gln
 275 280 285

10 Thr Glu Lys Ala Val Glu Asp Phe Leu Arg Ser Ile Gly Arg Ser Lys
 290 295 300

Lys Glu Arg Arg Pro Val Arg Pro His Thr Val Glu Lys Pro Val Pro
 305 310 315 320
 15 Ser Ser Ser Gly Gly Asp Ala His Val Pro His Gly Ser Gln Val Ile
 325 330 335

20 Arg Lys Leu Val Met Glu Pro Thr Phe Lys Pro Trp Gln Met Lys Thr
 340 345 350

His Phe Leu Met Pro Phe Pro Val Asn Tyr Val Gly Glu Cys Ile Arg
 355 360 365
 25

Thr Val Pro Tyr Thr Asp Pro Asp His Ala Ser Leu Lys Ile Leu Ala
 370 375 380
 30

Arg Leu Met Thr Ala Lys Phe Leu His Thr Glu Ile Arg Glu Lys Gly
 385 390 395 400

35 Gly Ala Tyr Gly Gly Gly Ala Lys Leu Ser His Asn Gly Ile Phe Thr
 405 410 415

40 Leu Tyr Ser Tyr Arg Asp Pro Asn Thr Ile Glu Thr Leu Gln Ser Phe
 420 425 430

Gly Lys Ala Val Asp Trp Ala Lys Ser Gly Lys Phe Thr Gln Gln Asp
 435 440 445
 45

Ile Asp Glu Ala Lys Leu Ser Val Phe Ser Thr Val Asp Ala Pro Val
 450 455 460
 50

Ala Pro Ser Asp Lys Gly Met Asp His Phe Leu Tyr Gly Leu Ser Asp
 465 470 475 480

55 Glu Met Lys Gln Ala His Arg Glu Gln Leu Phe Ala Val Ser His Asp
 485 490 495

Lys Leu Leu Ala Val Ser Asp Arg Tyr Leu Gly Thr Gly Lys Ser Thr

51/67

500

505

510

5 His Gly Leu Ala Ile Leu Gly Pro Glu Asn Pro Lys Ile Ala Lys Asp
 515 520 525

10 Pro Ser Trp Ile Ile Arg
 530

<210> 14
 <211> 409
 15 <212> PRT
 <213> Bacillus subtilis
 <400> 14

20 Met Ile Lys Arg Tyr Thr Cys Pro Asn Gly Val Arg Ile Val Leu Glu
 1 5 10 15

25 Asn Asn Pro Thr Val Arg Ser Val Ala Ile Gly Val Trp Ile Gly Thr
 20 25 30

30 Gly Ser Arg His Glu Thr Pro Glu Ile Asn Gly Ile Ser His Phe Leu
 35 40 45

Glu His Met Phe Phe Lys Gly Thr Ser Thr Lys Ser Ala Arg Glu Ile
 50 55 60

35 Ala Glu Ser Phe Asp Arg Ile Gly Gly Gln Val Asn Ala Phe Thr Ser
 65 70 75 80

40 Lys Glu Tyr Thr Cys Tyr Tyr Ala Lys Val Leu Asp Glu His Ala Asn
 85 90 95

45 Tyr Ala Leu Asp Val Leu Ala Asp Met Phe Phe His Ser Thr Phe Asp
 100 105 110

50 Glu Asn Glu Leu Lys Lys Glu Lys Asn Val Val Tyr Glu Glu Ile Lys
 115 120 125

Met Tyr Glu Asp Ala Pro Asp Asp Ile Val His Asp Leu Leu Ser Lys
 130 135 140

55 Ala Thr Tyr Gly Asn His Ser Leu Gly Tyr Pro Ile Leu Gly Thr Glu
 145 150 155 160

52/67

Glu Thr Leu Ala Ser Phe Asn Gly Asp Ser Leu Arg Gln Tyr Met His
165 170 175

5 Asp Tyr Tyr Thr Pro Asp Arg Val Val Ile Ser Val Ala Gly Asn Ile
180 185 190

10 Ser Asp Ser Phe Ile Lys Asp Val Glu Lys Trp Phe Gly Ser Tyr Glu
195 200 205

Ala Lys Gly Lys Ala Thr Gly Leu Glu Lys Pro Glu Phe His Thr Glu
210 215 220

15 Lys Leu Thr Arg Lys Lys Glu Thr Glu Gln Ala His Leu Cys Leu Gly
225 230 235 240

20 Phe Lys Gly Leu Glu Val Gly His Glu Arg Ile Tyr Asp Leu Ile Val
245 250 255

25 Leu Asn Asn Val Leu Gly Gly Ser Met Ser Ser Arg Leu Phe Gln Asp
260 265 270

Val Arg Glu Asp Lys Gly Leu Ala Tyr Ser Val Tyr Ser Tyr His Ser
275 280 285

30 Ser Tyr Glu Asp Ser Gly Met Leu Thr Ile Tyr Gly Gly Thr Gly Ala
290 295 300

35 Asn Gln Leu Gln Gln Leu Ser Glu Thr Ile Gln Glu Thr Leu Ala Thr
305 310 315 320

40 Leu Lys Arg Asp Gly Ile Thr Ser Lys Glu Leu Glu Asn Ser Lys Glu
325 330 335

45 Gln Met Lys Gly Ser Leu Met Leu Ser Leu Glu Ser Thr Asn Ser Lys
340 345 350

Met Ser Arg Asn Gly Lys Asn Glu Leu Leu Leu Gly Lys His Lys Thr
355 360 365

50 Leu Asp Glu Ile Ile Asn Glu Leu Asn Ala Val Asn Leu Glu Arg Val
370 375 380

55 Asn Gly Leu Ala Arg Gln Leu Phe Thr Glu Asp Tyr Ala Leu Ala Leu
385 390 395 400

53/67

Ile Ser Pro Ser Gly Asn Met Pro Ser
405

5 <210> 15

<211> 438

<212> PRT

<213> Mycobacterium tuberculosis

10 <400> 15

Met Pro Arg Arg Ser Pro Ala Asp Pro Ala Ala Ala Leu Ala Pro Arg
1 5 10 15

15 Arg Thr Thr Leu Pro Gly Gly Leu Arg Val Val Thr Glu Phe Leu Pro
20 25 30

Ala Val His Ser Ala Ser Val Gly Val Trp Val Gly Val Gly Ser Arg
20 35 40 45

Asp Glu Gly Ala Thr Val Ala Gly Ala Ala His Phe Leu Glu His Leu
25 50 55 60

Leu Phe Lys Ser Thr Pro Thr Arg Ser Ala Val Asp Ile Ala Gln Ala
65 70 75 80

30

Met Asp Ala Val Gly Gly Glu Leu Asn Ala Phe Thr Ala Lys Glu His
85 90 95

35 Thr Cys Tyr Tyr Ala His Val Leu Gly Ser Asp Leu Pro Leu Ala Val
100 105 110

Asp Leu Val Ala Asp Val Val Leu Asn Gly Arg Cys Ala Ala Asp Asp
40 115 120 125

Val Glu Val Glu Arg Asp Val Val Leu Glu Glu Ile Ala Met Arg Asp
45 130 135 140

Asp Asp Pro Glu Asp Ala Leu Ala Asp Met Phe Leu Ala Ala Leu Phe
145 150 155 160

50

Gly Asp His Pro Val Gly Arg Pro Val Ile Gly Ser Ala Gln Ser Val
165 170 175

55 Ser Val Met Thr Arg Ala Gln Leu Gln Ser Phe His Leu Arg Arg Tyr
180 185 190

Thr Pro Glu Arg Met Val Val Ala Ala Ala Gly Asn Val Asp His Asp

54/67

	195	200	205
5	Gly Leu Val Ala Leu Val Arg 210	Glu His Phe Gly Ser Arg 215	Leu Val Arg 220
10	Gly Arg Arg Pro Val Ala Pro Arg Lys Gly Thr Gly Arg Val Asn Gly 225 230 235 240	Ser Pro Arg Leu Thr Leu Val Ser Arg Asp Ala Glu Gln Thr His Val 245 250 255	
15	Ser Leu Gly Ile Arg Thr Pro Gly Arg Gly Trp Glu His Arg Trp Ala 260 265 270		
20	Leu Ser Val Leu His Thr Ala Leu Gly Gly Gly Leu Ser Ser Arg Leu 275 280 285		
25	Phe Gln Glu Val Arg Glu Thr Arg Gly Leu Ala Tyr Ser Val Tyr Ser 290 295 300		
30	Ala Leu Asp Leu Phe Ala Asp Ser Gly Ala Leu Ser Val Tyr Ala Ala 305 310 315 320		
35	Cys Leu Pro Glu Arg Phe Ala Asp Val Met Arg Val Thr Ala Asp Val 325 330 335		
40	Leu Glu Ser Val Ala Arg Asp Gly Ile Thr Glu Ala Glu Cys Gly Ile 340 345 350		
45	Ala Lys Gly Ser Leu Arg Gly Gly Leu Val Leu Gly Leu Glu Asp Ser 355 360 365		
50	Ser Ser Arg Met Ser Arg Leu Gly Arg Ser Glu Leu Asn Tyr Gly Lys 370 375 380		
55	His Arg Ser Ile Glu His Thr Leu Arg Gln Ile Glu Gln Val Thr Val 385 390 395 400		
	Glu Glu Val Asn Ala Val Ala Arg His Leu Leu Ser Arg Arg Tyr Gly 405 410 415		
	Ala Ala Val Leu Gly Pro His Gly Ser Lys Arg Ser Leu Pro Gln Gln 420 425 430		
	Leu Arg Ala Met Val Gly 435		

55/67

<210> 16
<211> 34
5 <212> DNA
<213> Artificial Sequence

<220>
10 <223> Oligonucleotide

<400> 16
aatagaagct tgtcgactga tctatccaaa actg 34

15
<210> 17
<211> 66
<212> DNA
<213> Artificial Sequence

20
<220>
<223> Oligonucleotide

<400> 17
25 aaaagagctc ggccagatct tctagaggat ccaagaattc tgttttatat ttgttgtaaa 60
aagtag 66

30 <210> 18
<211> 37
<212> DNA
<213> Artificial Sequence

35
<220>
<223> Oligonucleotide

<400> 18
40 ttttgaattc caagatctcc catgtctcta ctggtgg 37

<210> 19
<211> 41
45 <212> DNA
<213> Artificial Sequence

<220>
50 <223> Oligonucleotide

<400> 19
ccccgagctc gtcgaccctt ctcgaaagct ttaacgaacg c 41

55
<210> 20
<211> 43
<212> DNA
<213> Artificial Sequence

56/67

<220>
<223> Oligonucleotide

5 <400> 20
ttttgaattc aaagaatgag atttccttca atttttactg cag 43

<210> 21
<211> 37
10 <212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

15 <400> 21
tttttctaga ctaggagggg tactcatact cctcggc 37

<210> 22
20 <211> 33
<212> DNA
<213> Artificial Sequence

<220>
25 <223> Oligonucleotide

<400> 22
cgaatgtcca tcgttgcgaa cctgcagaac ctg 33

30 <210> 23
<211> 33
<212> DNA
<213> Artificial Sequence

35 <220>
<223> Oligonucleotide

<400> 23
40 caggttctgc aggttcctaa cgatggacat tcg 33

<210> 24
<211> 33
<212> DNA
<213> Artificial Sequence

45 <220>
<223> Oligonucleotide

<400> 24
50 cgaatgtcca tcgttaggaa cctgcagaac ctg 33

<210> 25
<211> 33
55 <212> DNA
<213> Artificial Sequence

<220>

57/67

<223> Oligonucleotide

<400> 25
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5 <210> 26
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<213> Artificial Sequence

10 <220>
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<400> 26
tcgcagagaa cggatggc 18

15 <210> 27
<211> 36
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20 <213> Artificial Sequence

<220>
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25 <400> 27
ttttgggcc ttcattgtga tacggtatct cttggc 36

<210> 28
30 <211> 37
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<220>
35 <223> Oligonucleotide

<400> 28
ttttctcgag aaggtggaac atactgccct gggatgg 37

40 <210> 29
<211> 38
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<213> Artificial Sequence

45 <220>
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<400> 29
50 ttttgagctc gtttaggaaa cgtccttggc ggagatgc 38

<210> 30
<211> 40
55 <212> DNA
<213> Artificial Sequence

<220>
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<400> 30
tttttctaga cactgcgaat ccatggtata aaccaaacc 40
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5 <211> 24
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<220>
10 <223> Oligonucleotide

<400> 31
gtcgttggtc atggacatac ctcc 24
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<210> 32
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<400> 32
25 tacaaatggtt cttctgcat ttctgg 26

<210> 33
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30 <212> DNA
<213> Artificial Sequence

<220>
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35 <400> 33
ggttcatatg cgccggagct cctcgacagc ag 32

40 <210> 34
<211> 37
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45 <220>
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<400> 34
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<210> 35
<211> 70
<212> DNA
55 <213> Artificial Sequence

<220>
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59/67

<400> 35
ttaaagagta ccttggctat agaataccgt agagataaag acctgaatag agattgtact 60
gagagtgcac 70

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15 aggtattata actatttttc tgtatttttt atatattttt atttgccaag ctgtgcggtata 60
tttcacaccg 70

20 <210> 37
<211> 23
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25 <220>
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<400> 37
30 ctttgggttaa agagtacctt ggc 23

<210> 38
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40 <400> 38
tactacgaaa agcgtgtgcg agg 23

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55 tgagagtgca c 71

60/67

<210> 40
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15 <210> 41
 <211> 22
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 25 cggaggggct ctatgataaa gg 22

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 35 <400> 42
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<210> 43
 40 <211> 85
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Ser Gly Leu Gln Arg Ala Glu Glu Ala Pro Arg Arg Gln Leu Arg Val
 1 5 10 15

50 Ser Gln Arg Thr Asp Gly Glu Ser Arg Ala His Leu Gly Ala Leu Leu
 20 25 30

Ala Arg Tyr Ile Gln Gln Ala Arg Lys Ala Pro Ser Gly Arg Met Ser
 55 35 40 45

Ile Val Lys Asn Leu Gln Asn Leu Asp Pro Ser His Arg Ile Ser Asp
 50 55 60

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Arg Asp Tyr Met Gly Trp Met Asp Phe Gly Arg Arg Ser Ala Glu Glu
 65 70 75 80

5

Tyr Glu Tyr Pro Ser
 85

10

<210> 44
 <211> 22
 <212> PRT
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<400> 44

Gln Leu Arg Val Ser Gln Arg Thr Asp Gly Glu Ser Arg Ala His Leu
 20 1 5 10 15

Gly Ala Leu Leu Ala Arg
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25

<210> 45
 <211> 19
 <212> PRT
 30 <213> Homo sapiens

<400> 45

35 Val Ser Gln Arg Thr Asp Gly Glu Ser Arg Ala His Leu Gly Ala Leu
 1 5 10 15

Leu Ala Arg

40

<210> 46
 <211> 51
 45 <212> PRT
 <213> Homo sapiens

<400> 46

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Tyr Ile Gln Gln Ala Arg Lys Ala Pro Ser Gly Arg Met Ser Ile Val
 1 5 10 15

55 Lys Asn Leu Gln Asn Leu Asp Pro Ser His Arg Ile Ser Asp Arg Asp
 20 25 30
 Tyr Met Gly Trp Met Asp Phe Gly Arg Arg Ser Ala Glu Glu Tyr Glu
 35 40 45

62/67

Tyr Pro Ser
50

5 <210> 47
<211> 17
<212> PRT
<213> Homo sapiens

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<400> 47

Tyr Ile Gln Gln Ala Arg Lys Ala Pro Ser Gly Arg Met Ser Ile Val
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15
Lys

20 <210> 48
<211> 16
<212> PRT
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25 <400> 48

Tyr Ile Gln Gln Ala Arg Lys Ala Pro Ser Gly Arg Met Ser Ile Val
1 5 10 15

30 <210> 49
<211> 13
<212> PRT
<213> Homo sapiens

35
<400> 49

Asn Leu Gln Asn Leu Asp Pro Ser His Arg Ile Ser Asp
1 5 10

40
<210> 50
<211> 23
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45 <213> Homo sapiens

<400> 50

50 Asn Leu Gln Asn Leu Asp Pro Ser His Arg Ile Ser Asp Arg Asp Tyr
1 5 10 15

Met Gly Trp Met Asp Phe Gly
55 20

<210> 51
<211> 34
<212> PRT
<213> Homo sapiens

63/67

<400> 51

Asn Leu Gln Asn Leu Asp Pro Ser His Arg Ile Ser Asp Arg Asp Tyr
5 1 5 10 15

Met Gly Trp Met Asp Phe Gly Arg Arg Ser Ala Glu Glu Tyr Glu Tyr
20 25 30
10

Pro Ser

15

<210> 53
<211> 12
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20

<220>
<223> Portion of fusion protein

<400> 53

25

Lys Arg Glu Ala Glu Ala Ser Gly Leu Gln Arg Ala
1 5 10

30

<210> 54
<211> 9
<212> PRT
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35

<400> 54

Arg Met Ser Ile Val Lys Asn Leu Gln
1 5

40

<210> 55
<211> 13
<212> PRT
45 <213> Homo sapiens

<400> 55

Asp Arg Asp Tyr Met Gly Trp Met Asp Phe Gly Arg Arg
50 1 5 10

<210> 56
<211> 48
55 <212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide MFalBNP (S)

64/67

<400> 56
5 ggataaaaga gaggtgaag ctcacccgct gggcagcccc gggtcagc 48
<210> 57
<211> 48
<212> DNA
<213> Artificial Sequence
10
<220>
<223> MF1aBNP (AS)
<400> 57
15 gctgaaccgg ggctgcccag cgggtgagct tcagcctctc ttttatcc 48
<210> 58
<211> 34
<212> DNA
20 <213> Artificial Sequence
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<400> 58
tttgaattc atggatcccc agacagcacc ttcc 34
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30 <211> 33
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35 <223> Oligonucleotide BNP3'XbaI
<400> 59
40 ttttctaga ttaatgccgc ctcagcactt tgc 33
<210> 60
<211> 48
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<400> 60
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<210> 61
<211> 48
55 <212> DNA
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<220>
<223> Oligonucleotide MF1BNP (AS)

65/67

<400> 61
5 gctgaaccgg ggctgcccag cgggtgagct tcagcctctc ttttatcc 48

<210> 62
<211> 69
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<213> Artificial Sequence

10 <220>
<223> Oligonucleotide YPS15'GD400

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agagtgcac 69

<210> 63
<211> 70
20 <212> DNA
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<220>
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tttcacaccg 70

30 <210> 64
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<212> DNA
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35 <220>
<223> Oligonucleotide YPS15'DC

<400> 64
40 tcgtttcact gatgtgtccg 20

<210> 65
<211> 21
<212> DNA
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<400> 65
50 gattataggc catatcccag g 21

<210> 66
<211> 13
<212> PRT
55 <213> Artificial Sequence

<220>
<223> Pitrilysin consensus sequence

66/67

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 <222> (1)...(13)
 <223> Xaa = Any Amino Acid
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 <223> Xaa = Any Amino Acid
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 15 <222> (0)...(0)
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 1 5 10
 20
 <210> 67
 <211> 44
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 40 <222> (1)...(44)
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 <222> (34)...(34)
 45 <223> Xaa = any amino acid or absent
 <221> VARIANT
 <222> (35)...(35)
 <223> Xaa = any amino acid or absent
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 <400> 12
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 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 55 Xaa Xaa Xaa Asn Ala Xaa Thr Xaa Xaa Xaa Xaa Thr
 35 40

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<210> 68
<211> 44
<212> PRT
<213> Artificial Sequence
5
<220>
<223> Pitrilysin consensus sequence

10 <221> VARIANT
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<223> Xaa = Any Amino Acid

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15 <222> (1)...(44)
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20 <223> Xaa = Any Amino Acid

<221> VARIANT
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<223> Xaa = any amino acid or absent
25

<221> VARIANT
<222> (35)...(35)
<223> Xaa = any amino acid or absent

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1 5 10 15
Tyr Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
20 25 30
35 Xaa Xaa Xaa Asn Ala Xaa Thr Xaa Xaa Xaa Xaa Thr
35 40

